OIPE

SEQUENCE LISTING
```
 3 (1) GENERAL INFORMATION:
 5       (i) APPLICANT: SAMSON, MICHEL
 6                      PARMENTIER, MARC
 7                      VASSART, GILBERT
 8                      LIBERT, FREDERICK
10      (ii) TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
11                      AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR
13     (iii) NUMBER OF SEQUENCES: 17
15      (iv) CORRESPONDENCE ADDRESS:
16           (A) ADDRESSEE: Knobbe, Martens, Olson & Bear
17           (B) STREET: 620 Newport Center Drive 16th Floor
18           (C) CITY: Newport Beach
19           (D) STATE: CA
20           (E) COUNTRY: U.S.A.
21           (F) ZIP: 92660
23       (v) COMPUTER READABLE FORM:
24           (A) MEDIUM TYPE: Floppy disk
25           (B) COMPUTER: IBM PC compatible
26           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27           (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
29      (vi) CURRENT APPLICATION DATA:
C--> 30      (A) APPLICATION NUMBER: US/09/938,703
C--> 31      (B) FILING DATE: 24-Aug-2001
32           (C) CLASSIFICATION:
35     (vii) PRIOR APPLICATION DATA:
36           (A) APPLICATION NUMBER: 09/626,939
37           (B) FILING DATE: 2000-07-27
42    (viii) ATTORNEY/AGENT INFORMATION:
43           (A) NAME: Altman, Daniel E
44           (B) REGISTRATION NUMBER: 34,115
45           (C) REFERENCE/DOCKET NUMBER:
47 (2) INFORMATION FOR SEQ ID NO: 1:
49       (i) SEQUENCE CHARACTERISTICS:
50           (A) LENGTH: 792 base pairs
51           (B) TYPE: nucleic acid
52           (C) STRANDEDNESS: single
53           (D) TOPOLOGY: linear
55      (ii) MOLECULE TYPE: DNA (genomic)
58      (ix) FEATURE:
59           (A) NAME/KEY: CDS
60           (B) LOCATION: 240..791
63      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
65 GAATTCCCCC AACAGAGCCA AGCTCTCCAT CTAGTGGACA GGGAAGCTAG CAGCAAACCT        60
66 TCCCTTCACT ACAAAACTTC ATTGCTTGGC CAAAAGAGA GTTAATTCAA TGTAGACATC        120
67 TATGTAGGCA ATTAAAAACC TATTGATGTA TAAAACAGTT TGCATTCATG GAGGGCAACT        180
68 AAATACATTC TAGGACTTTA TAAAAGATCA CTTTTTATTT ATGCACAGGG TGGAACAAG         239
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69 ATG GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC ATC AAT TAT TAT ACA      287
70 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
71  1               5                  10                  15
72 TCG GAG CCC TGC CAA AAA ATC AAT GTG AAG CAA ATC GCA GCC CGC CTC      335
73 Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
74          20                  25                  30
75 CTG CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT GGT TTT GTG GGC AAC      383
76 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
77          35                  40                  45
78 ATG CTG GTC ATC CTC ATC CTG ATA AAC TGC AAA AGG CTG AAG AGC ATG      431
79 Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
80      50                  55                  60
81 ACT GAC ATC TAC CTG CTC AAC CTG GCC ATC TCT GAC CTG TTT TTC CTT      479
82 Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
83  65                  70                  75                  80
84 CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC GCC CAG TGG GAC TTT      527
85 Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
86                  85                  90                  95
87 GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC TAT TTT ATA GGC TTC      575
88 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
89              100                 105                 110
90 TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG      623
91 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
92          115                 120                 125
93 GCT GTC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT      671
94 Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
95      130                 135                 140
96 GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GCT GTG TTT GCG TCT      719
97 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
98 145                 150                 155                 160
99 CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC      767
100 Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
101                 165                 170                 175
102 ACC TGC AGC TCT CAT TTT CCA TAC A                                   792
103 Thr Cys Ser Ser His Phe Pro Tyr
104              180
107 (2) INFORMATION FOR SEQ ID NO: 2:
109     (i) SEQUENCE CHARACTERISTICS:
110         (A) LENGTH: 1477 base pairs
111         (B) TYPE: nucleic acid
112         (C) STRANDEDNESS: single
113         (D) TOPOLOGY: linear
115    (ii) MOLECULE TYPE: DNA (genomic)
118    (ix) FEATURE:
119         (A) NAME/KEY: CDS
120         (B) LOCATION: 240..1295
123    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
125 GAATTCCCCC AACAGAGCCA AGCTCTCCAT CTAGTGGACA GGGAAGCTAG CAGCAAACCT   60
126 TCCCTTCACT ACAAAACTTC ATTGCTTGGC CAAAAAGAGA GTTAATTCAA TGTAGACATC   120
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RAW SEQUENCE LISTING   DATE: 12/19/2001
PATENT APPLICATION: US/09/938,703   TIME: 12:44:35

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Output Set: N:\CRF3\12192001\I938703.raw

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127 TATGTAGGCA ATTAAAAACC TATTGATGTA TAAAACAGTT TGCATTCATG GAGGGCAACT      180
128 AAATACATTC TAGGACTTTA TAAAAGATCA CTTTTTATTT ATGCACAGGG TGGAACAAG       239
129 ATG GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC ATC AAT TAT TAT ACA        287
130 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
131   1               5                   10                  15
132 TCG GAG CCC TGC CAA AAA ATC AAT GTG AAG CAA ATC GCA GCC CGC CTC        335
133 Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
134          20                  25                  30
135 CTG CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT GGT TTT GTG GGC AAC        383
136 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
137          35                  40                  45
138 ATG CTG GTC ATC CTC ATC CTG ATA AAC TGC AAA AGG CTG AAG AGC ATG        431
139 Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
140      50                  55                  60
141 ACT GAC ATC TAC CTG CTC AAC CTG GCC ATC TCT GAC CTG TTT TTC CTT        479
142 Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
143 65                  70                  75                  80
144 CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC GCC CAG TGG GAC TTT        527
145 Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
146              85                  90                  95
147 GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC TAT TTT ATA GGC TTC        575
148 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
149              100                 105                 110
150 TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG        623
151 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
152          115                 120                 125
153 GCT GTC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT        671
154 Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
155      130                 135                 140
156 GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GCT GTG TTT GCG TCT        719
157 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
158 145                 150                 155                 160
159 CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC        767
160 Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
161              165                 170                 175
162 ACC TGC AGC TCT CAT TTT CCA TAC AGT CAG TAT CAA TTC TGG AAG AAT        815
163 Thr Cys Ser Ser His Phe Pro Tyr Ser Gln Tyr Gln Phe Trp Lys Asn
164              180                 185                 190
165 TTC CAG ACA TTA AAG ATA GTC ATC TTG GGG CTG GTC CTG CCG CTG CTT        863
166 Phe Gln Thr Leu Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu
167          195                 200                 205
168 GTC ATG GTC ATC TGC TAC TCG GGA ATC CTA AAA ACT CTG CTT CGG TGT        911
169 Val Met Val Ile Cys Tyr Ser Gly Ile Leu Lys Thr Leu Leu Arg Cys
170      210                 215                 220
171 CGA AAT GAG AAG AAG AGG CAC AGG GCT GTG AGG CTT ATC TTC ACC ATC        959
172 Arg Asn Glu Lys Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile
173 225                 230                 235                 240
174 ATG ATT GTT TAT TTT CTC TTC TGG GCT CCC TAC AAC ATT GTC CTT CTC       1007
175 Met Ile Val Tyr Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu
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Input Set : N:\Crf3\RULE60\09938703.txt
Output Set: N:\CRF3\12192001\I938703.raw

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176                245               250               255
177 CTG AAC ACC TTC CAG GAA TTC TTT GGC CTG AAT AAT TGC AGT AGC TCT    1055
178 Leu Asn Thr Phe Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser
179                260               265               270
180 AAC AGG TTG GAC CAA GCT ATG CAG GTG ACA GAG ACT CTT GGG ATG ACG    1103
181 Asn Arg Leu Asp Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr
182                275               280               285
183 CAC TGC TGC ATC AAC CCC ATC ATC TAT GCC TTT GTC GGG GAG AAG TTC    1151
184 His Cys Cys Ile Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe
185        290               295               300
186 AGA AAC TAC CTC TTA GTC TTC TTC CAA AAG CAC ATT GCC AAA CGC TTC    1199
187 Arg Asn Tyr Leu Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe
188 305                310               315               320
189 TGC AAA TGC TGT TCT ATT TTC CAG CAA GAG GCT CCC GAG CGA GCA AGC    1247
190 Cys Lys Cys Cys Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser
191                325               330               335
192 TCA GTT TAC ACC CGA TCC ACT GGG GAG CAG GAA ATA TCT GTG GGC TTG    1295
193 Ser Val Tyr Thr Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu
194                340               345               350
195 TGACACGGAC TCAAGTGGGC TGGTGACCCA GTCAGAGTTG TGCACATGGC TTAGTTTTCA    1355
196 TACACAGCCT GGGCTGGGGG TNGGTTGGNN GAGGTCTTTT TTAAAAGGAA GTTACTGTTA    1415
197 TAGAGGGTCT AAGATTCATC CATTTATTTG GCATCTGTTT AAAGTAGATT AGATCCGAAT    1475
198 TC                                                                  1477
201 (2) INFORMATION FOR SEQ ID NO: 3:
203        (i) SEQUENCE CHARACTERISTICS:
204                (A) LENGTH: 1442 base pairs
205                (B) TYPE: nucleic acid
206                (C) STRANDEDNESS: single
207                (D) TOPOLOGY: linear
209        (ii) MOLECULE TYPE: DNA (genomic)
212        (ix) FEATURE:
213                (A) NAME/KEY: CDS
214                (B) LOCATION: 240..884
217        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
219 GAATTCCCCC AACAGAGCCA AGCTCTCCAT CTAGTGGACA GGGAAGCTAG CAGCAAACCT      60
220 TCCCTTCACT ACAAAACTTC ATTGCTTGGC CAAAAAGAGA GTTAATTCAA TGTAGACATC     120
221 TATGTAGGCA ATTAAAAACC TATTGATGTA TAAAACAGTT TGCATTCATG GAGGGCAACT     180
222 AAATACATTC TAGGACTTTA TAAAAGATCA CTTTTTATTT ATGCACAGGG TGGAACAAG      239
223 ATG GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC ATC AAT TAT TAT ACA      287
224 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
225   1                5                  10                 15
226 TCG GAG CCC TGC CAA AAA ATC AAT GTG AAG CAA ATC GCA GCC CGC CTC      335
227 Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
228        20               25                30
229 CTG CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT GGT TTT GTG GGC AAC      383
230 Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
231        35               40                45
232 ATG CTG GTC ATC CTC ATC CTG ATA AAC TGC AAA AGG CTG AAG AGC ATG      431
233 Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
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RAW SEQUENCE LISTING   DATE: 12/19/2001
PATENT APPLICATION: US/09/938,703   TIME: 12:44:35

Input Set : N:\Crf3\RULE60\09938703.txt
Output Set: N:\CRF3\12192001\I938703.raw

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234      50                      55                      60
235 ACT GAC ATC TAC CTG CTC AAC CTG GCC ATC TCT GAC CTG TTT TTC CTT      479
236 Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
237 65                      70                      75                      80
238 CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC GCC CAG TGG GAC TTT      527
239 Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
240                      85                      90                      95
241 GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC TAT TTT ATA GGC TTC      575
242 Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
243              100                     105                     110
244 TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG      623
245 Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
246         115                     120                     125
247 GCT GTC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT      671
248 Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
249      130                     135                     140
250 GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GCT GTG TTT GCG TCT      719
251 Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
252 145                     150                     155                     160
253 CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC      767
254 Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
255                     165                     170                     175
256 ACC TGC AGC TCT CAT TTT CCA TAC ATT AAA GAT AGT CAT CTT GGG GCT      815
257 Thr Cys Ser Ser His Phe Pro Tyr Ile Lys Asp Ser His Leu Gly Ala
258             180                     185                     190
259 GGT CCT GCC GCT GCT TGT CAT GGT CAT CTG CTA CTC GGG AAT CCT AAA      863
260 Gly Pro Ala Ala Ala Cys His Gly His Leu Leu Leu Gly Asn Pro Lys
261         195                     200                     205
262 AAC TCT GCT TCG GTG TCG AAA TGAGAAGAAG AGGCACAGGG CTGTGAGGCT      914
263 Asn Ser Ala Ser Val Ser Lys
264      210                     215
265 TATCTTCACC ATCATGATTG TTTATTTTCT CTTCTGGGCT CCCTACAACA TTGTCCTTCT      974
266 CCTGAACACC TTCCAGGAAT TCTTTGGCCT GAATAATTGC AGTAGCTCTA ACAGGTTGGA     1034
267 CCAAGCTATG CAGGTGACAG AGACTCTTGG GATGACGCAC TGCTGCATCA ACCCCATCAT     1094
268 CTATGCCTTT GTCGGGGAGA AGTTCAGAAA CTACCTCTTA GTCTTCTTCC AAAAGCACAT     1154
269 TGCCAAACGC TTCTGCAAAT GCTGTTCTAT TTTCCAGCAA GAGGCTCCCG AGCGAGCAAG     1214
270 CTCAGTTTAC ACCCGATCCA CTGGGGAGCA GGAAATATCT GTGGGCTTGT GACACGGACT     1274
271 CAAGTGGGCT GGTGACCCAG TCAGAGTTGT GCACATGGCT TAGTTTTCAT ACACAGCCTG     1334
272 GGCTGGGGGT GGTTGGGAGG TCTTTTTTAA AAGGAAGTTA CTGTTATAGA GGGTCTAAGA     1394
273 TTCATCCATT TATTTGGCAT CTGTTAAAG TAGATTAGAT CCGAATTC                  1442
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276 (2) INFORMATION FOR SEQ ID NO: 4:
278   (i) SEQUENCE CHARACTERISTICS:
279   (A) LENGTH: 184 amino acids
280   (B) TYPE: amino acid
281   (D) TOPOLOGY: linear
283   (ii) MOLECULE TYPE: protein
285   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
287 Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
288 1   5   10   15

VERIFICATION SUMMARY   DATE: 12/19/2001
PATENT APPLICATION: US/09/938,703   TIME: 12:44:36

Input Set : **N:\Crf3\RULE60\09938703.txt**
Output Set: **N:\CRF3\12192001\I938703.raw**

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L:31  M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:418 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7
L:462 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:477 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=8
L:509 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:521 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:536 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=9
L:595 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=10
L:617 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:639 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
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